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DETECTION OF FIVE COMMONLY OCCURRED BRAIN DISEASES

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ABSTRACT

Life threatening diseases in both male and female are Brain tumor, stroke, hemorrhage and multiple sclerosis (MS). The most common and widespread disease among these brain diseases is Brain tumor. Early and accurate diagnosis of brain lesion is vital for determining accurate treatment and prognosis. However, the diagnosis is a very challenging task and can only be performed by specialists in neuroradiology. The aim of the paper is to detect brain tumour. All collected MRIs reports are diagnosed by radiologists of hospitals.

KEYWORDS: Brain Tumor, Glioma, Meningioma, Metastatic adenocarcinoma, Metastatic bronchogenic carcinoma, Sarcoma.

INTRODUCTION

Brain tumors forms the second most cause for cancer related deaths in children and adults. A tumor can be graded in to several stages in accordance to the analysis of abnormality of the tumor cells and tissues. This grading gives us the acute probability of tumor growth in size and its spreading. Tumor grade can be determined using biopsy. It is to be noted that grading of tumor is not same as cancer stages. The accurate diagnosis of brain tumors types is sometimes very difficult due to its high complexity and there are large variations. Five major types of brain tumors: 1) Glioma, 2) Meningioma, 3) Metastatic adenocarcinoma, 4) Metastatic bronchogenic carcinoma, and 5) Sarcoma are considered for computerized classification.[1] A database has been created that contains images associated with its corresponding class label. Images from this database were used in testing and training the classifiers.

In the first stage MRI image is taken as input and is normalized. The second stage includes extraction of feature vectors from the image which results in reducing redundancy of data to serve as the input to the classifier. The classification stage classifies the important feature for detection of tumour.[1]

Literature Review

The most important aim of brain MRI analysis is to extract clinical information that would improve diagnosis and treatment of disease. Extracting clinical information requires detection and segmentation of normal and abnormal tissues. In the recent days CAD system is used to enhance diagnostic capabilities of physicians and reduce the time required for accurate diagnosis.[2]

Computer aided detection of brain tumors, stroke lesions, hemorrhage lesions, and multiple sclerosis lesions are the most difficult issues in field of abnormal tissues segmentations because of many challenges.[3-5] The brain injuries are of varied shapes and also distort other normal and healthy tissues structures. Intensity distribution of normal tissues is very complicated and there exist some overlaps between different types of tissues. Over the last decade various approaches have been proposed for the same. Some researcher work on segmentation problem through machine learning methods. It is meant a well trained model that can determine whether a pixel belongs to a normal or abnormal tissue. Brain tumors are one of the most common brain diseases, so detection and segmentation of brain tumors in MRI are important in medical diagnosis.[6]

Supports Vector Machines (SVMs) are popular tools for classification by maximize the margin between classes of data that is independent and identically distributed. A SVM classification to classify the brain into the abnormal and normal classes using T1- weighted and contrast enhanced T1- weighted images.[7] This system used patient-specific training and compared classification of normal and abnormal using SVM classifier. It used the standard 2-class method and the more recent 1-class method.[8] The SVM method has the advantage of generalization and working in high dimensional feature space. It assumes that data are independently and identically distributed. Segmenting medical images with in-homogeneity and noise are creating problems of such classifiers.

Artificial neural network (ANN) is one of the powerful artificial intelligence techniques that have the capability to learn from a set of data and construct weight matrices to represent the

learning patterns. Each node in an ANNs is capable of performing elementary computations.[9] Neural networks represent both linear and nonlinear relationships and have the ability to learn these relationships directly from the data. Traditional linear models are simply inadequate since it contains nonlinear characteristics.[10] Because of the many interconnections used in a neural network, spatial information can be easily incorporated into its classification procedures.

Neural networks execute very well on complicated, difficult, multivariate non-linear domains, such as tumour, stroke, and hemorrhage segmentation where it becomes more difficult to use decision trees, or rule-based systems. They also perform a little better on noisy fields and there is no need to assume a fundamental data allocation such as usually done in statistical modelling.

Patients with brain tumours comprise a heterogeneous group with regard to age, symptom severity and prognosis. One should consider the best possible timing of surgery or oncological therapy. The risk to the patient increases if treatment is delayed.

Data Set

Dataset is a collection of similar and related data stored for processing. Further this can be defined as a collection of data that contains individual data units organized in a specific format. A data set generally contains a collection of a number of types of data. Medical dataset can be defined as a collection of pieces of information, especially those that are part of a collection to be used for the the diagnosis of diseases. In this paper data set, containing brain MRIs from from different Government hospitals as well as from Private Hospitals. Normally, hospitals stored the reports of patients MRIs prepared by radiologists. The hospitals provided all information for analysis due to the present scenario. The images are classified into normal, tends to be sign of tumour and also patients who already detected as brain cancer patients. These detections are based on the diagnosis of radiologists. The size of tumour is also classified according to the type of tumour present.

Proposed Method

Tumour detected MRI of brain slices is selected for classification. Artifacts and skull elimination is used to remove unnecessary regions of MRI. Next these are normalized to a range for feature extraction process. In the classification step, the model is first trained using training dataset obtained from the image database which also defines the class labels being

used. After performing the training on set of existing known data set then test the data for appropriate classes that help in correct medical decision making and diagnosis of brain tumour. The brief implementation of the technique has been shown in figure 1.

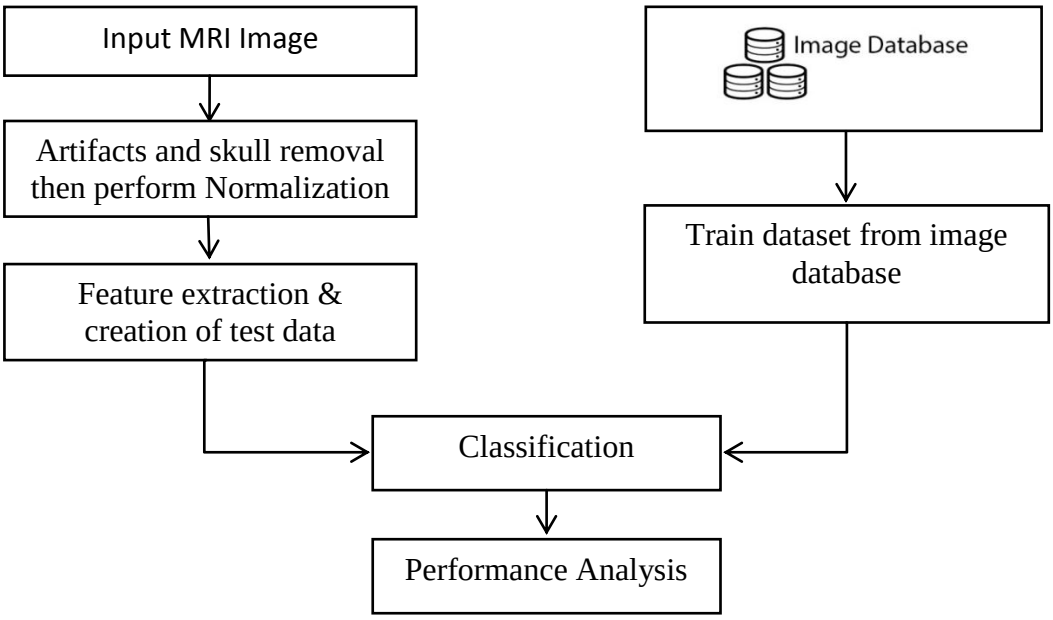

Figure 1: Workflow of the tumour classification.

Using above discussed parameters feature vector generates that can help in classification of the input image into the predetermined class label.

Classifications

Classification step occurs in two consecutive steps: learning phase and testing phase. The first one is known as training phase. It is the first step in classification. In this step it needs to build a model that can successfully classify a dataset. Back propagation algorithm is an optimization procedure based on gradient descent that adjusts the weights to reduce the system error. During the learning phase, input patterns are presented to the network and the network parameters are changed to bring the actual outputs closer to the desired target values. These outputs are compared to the target values. Any difference indicates an error. These errors are some scalar function of the weights. So the weights are to be adjusted for reducing the errors. This error function is the sum of square differences of the outputs and targets. Thus, the errors computed at the output layer are used to adjust the weights between the last hidden layer and the output layer.

The Artificial Neural Network System (ANFIS) uses fuzzy rules and fuzzy reasoning that is based on fuzzy set theory. It can also be said that fuzzy stands out to be a form of multi

valued logic. FIS is based upon the concepts of fuzzy set theory, fuzzy if-then rules and fuzzy reasoning. In case of fuzzy if-then rules which take the following form.

$if\ x\ is\ A\ then\ y\ is\ B$

Here A and B are linguistic values which is defined by fuzzy sets on the universe of discourse of X and Y respectively. The statement "$x\ is\ A$" is called the antecedent and the statement "yisB" is called the consequence. The relation between two variables x and y in which the fuzzy rule defined as a binary relation R on the product spaceX×Y. A fuzzy model can assume the following form of fuzzy rules.

$if\ x\ is\ A\ and\ y\ is\ B\ then\ z = f(x, y)$

Here A and B are fuzzy rules and z = f(x,y) is a crisp on the input variables x and y. A two input ANFIS has been shown in Figure 2.

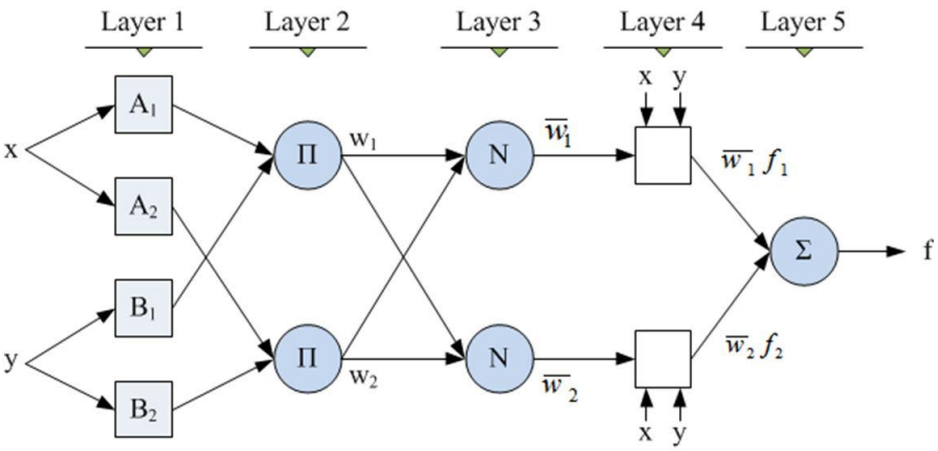

Figure 2: ANFIS architecture equivalent to fuzzy inference system.

In this model it has been observes that if a particular tuple does not match with the established fuzzy rules defined in the model, the classifier tries to give a result that is outside the solution set. This is helpful in determining a new type of tumour.

Results and Analysis

The images are normalized to the feature vector containing 12 features are extracted from the slices. Each of the feature vector forms an input tuple to the classifier. This vector is generated for 20 input slices shown in Figure 3 (Collected from hospitals) has been illustrated by Table 1 and Table 2.

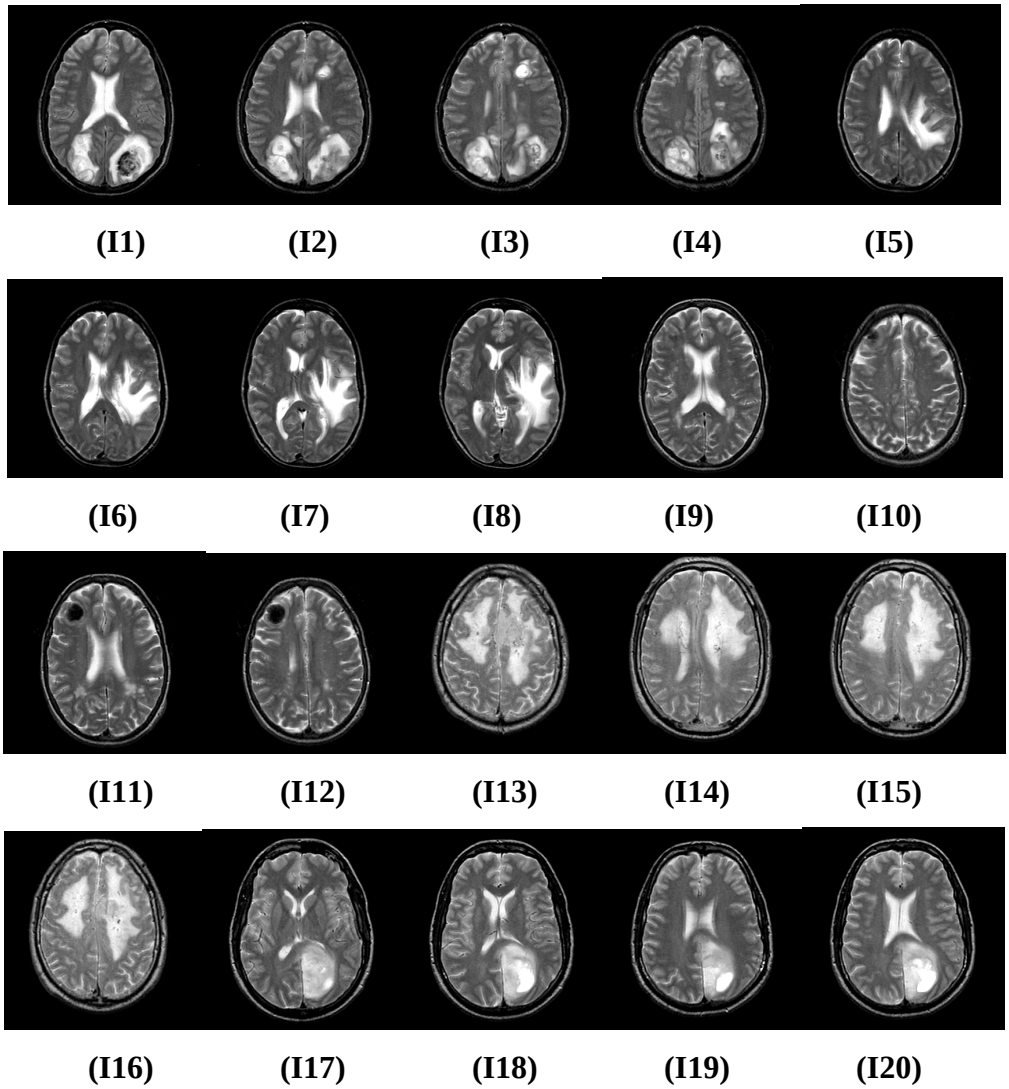

Figure 3: 20 input slices passed through the normalization and feature extraction processes for classification. After classification it is found that slices I1-I4 are Type 1 (Sarcoma); slicesI5-I8 are Type 2 (Meningioma); slices I9-I12 are Type 3 (Metastatic adenocarcinoma); slices I13-I16 are Type 4 (Metastatic bronchogenic carcinoma);slicesI17-I20 are Type 5 (Glioma).

Each of the generated feature vector from the normalized grayscale image are calculated from 1st order histogram based features and features from Gray Level Co-occurrence Matrix. Each of the functions derives a single valued element in the feature extraction matrix for each of the 20 slices that is represented in Table 1 and Table 2.

Table 1: Feature vector from the normalized grayscale MR image.

Image sequence	Mean	Variance	Skewness	Kurtosis	Energy	Entropy
1	15.5399	446.433	0.000108	0.000127	0.2816	3.6817
2	14.7607	427.681	0.000126	0.000151	0.2933	3.5751
3	15.5426	447.411	0.000108	0.000127	0.2810	3.6939
4	15.3294	434.847	0.000116	0.00014	0.2762	3.7014
5	15.9980	466.920	0.0001	0.000118	0.2718	3.8210
6	16.2995	455.317	0.000972	0.000117	0.2540	3.8918
7	16.8535	461.050	0.000906	0.00011	0.2365	3.9722
8	15.2010	463.274	0.000113	0.000132	0.2981	3.6796
9	13.6257	406.182	0.00015	0.000185	0.3333	3.2856
10	13.9531	413.331	0.000143	0.000175	0.3219	3.4029
11	13.1538	400.748	0.000161	0.000200	0.3529	3.2298
12	14.2234	417.177	0.000137	0.000165	0.3123	3.4526
13	13.6782	420.489	0.000142	0.000167	0.3506	3.2687
14	13.5103	417.582	0.000144	0.000169	0.3583	3.1849
15	13.2064	412.893	0.000151	0.000178	0.3698	3.1134
16	12.3658	388.257	0.000181	0.000226	0.3857	3.0153
17	12.9241	397.207	0.000167	0.00021	0.3573	3.2094
18	13.5875	407.496	0.000151	0.000185	0.3342	3.3352
19	14.2193	425.415	0.000137	0.000164	0.3174	3.4692
20	14.9834	443.361	0.000118	0.000138	0.3040	3.5664

Table 2: Feature vector of normalized grayscale MR image.

Image sequence	Contrast	Correlation	Energy	Homogeneity	Inverse difference	Absolute value
1	0.3334	0.3878	0.4131	0.8726	56710.6	17910
2	0.3190	0.3833	0.4379	0.8774	57036.6	17210
3	0.3415	0.3862	0.4071	0.8697	56512.8	18328
4	0.3547	0.3508	0.4112	0.8659	56247.2	18914
5	0.3618	0.3884	0.3971	0.8663	56246	18994
6	0.3499	0.3785	0.3871	0.8652	56218.6	18910
7	0.3697	0.3640	0.3731	0.8592	55806.6	19812
8	0.3610	0.3920	0.4227	0.8712	56534.6	18504
9	0.2931	0.3803	0.4756	0.8861	57632.2	15936
10	0.2984	0.3755	0.4668	0.8831	57439.6	16314
11	0.2885	0.3749	0.4930	0.8896	57854	15516
12	0.3019	0.3595	0.4589	0.8800	57245.4	16676
13	0.2558	0.4260	0.4907	0.8970	58395.4	14258
14	0.2565	0.4179	0.4908	0.8972	58406	14248
15	0.2443	0.4349	0.5019	0.9011	58674.6	13668
16	0.2395	0.4074	0.5274	0.9029	58796.6	13412
17	0.2881	0.3883	0.4918	0.8902	57893.2	15446
18	0.2936	0.3933	0.4727	0.8867	57670.4	15878
19	0.3158	0.3685	0.4617	0.8804	57227	16858
20	0.3164	0.3804	0.4429	0.8786	57115.6	17050

Each tuple contains its class label which denotes its tumour type which is used to build IF-THEN rules to generate the FIS. ANFIS is trained network that is used to generate the class label for the input slices. The class labels mentioned here were taken accordingly as: Class 1 = Sarcoma, Class 2 = Meningioma, Class 3 = Metastatic adenocarcinoma, Class 4 = Metastatic bronchogenic carcinoma, Class 5 = Glioma. The classifier gives fuzzy numbers as output which is de-fuzzified to get the crisp actual class labelled values.

Performance measurement

Performance is measured by comparing the actual class labels and the predicted class labels for each of the individual classifiers. In statistical analysis of classification, the F-score or F-measure is a measure of a test's accuracy. Performance measurement metrics value of 5 major tumour types as different class has been shown in Table 3.

Table 3: Performance measurement metrics value of 5 major tumour types.

Metric	Class 1	Class 2	Class 3	Class 4	Class 5
True Positive (TP)	37	43	32	29	48
False Negative (FN)	4	4	5	2	4
False Positive (FP)	3	3	2	6	5
True Negative (TN)	164	158	169	171	151
Sensitivity(TP/(TP+FN))	0.902	0.914	0.864	0.935	0.923
Specificity(TN/(FP+TN))	0.982	0.981	0.988	0.966	0.967
Precision(TP/(TP+FP))	0.925	0.934	0.941	0.828	0.905
Accuracy((TP+TN)/(P+N))	0.966	0.966	0.966	0.961	0.956
F score(2TP/(2P+FP+FN))	0.913	0.924	0.901	0.878	0.914

The performance of the classifiers is evaluated in terms of sensitivity, specificity, precision, accuracy and F score. The average value of sensitivity is 0.90815166, average value of specificity is 0.977151379, average value of precision is 0.907038177, average value of accuracy is 0.963461538, and average value of F score is 0.906558695 for an ANFIS. ROC curve of proposed system has been shown in Figure 4.

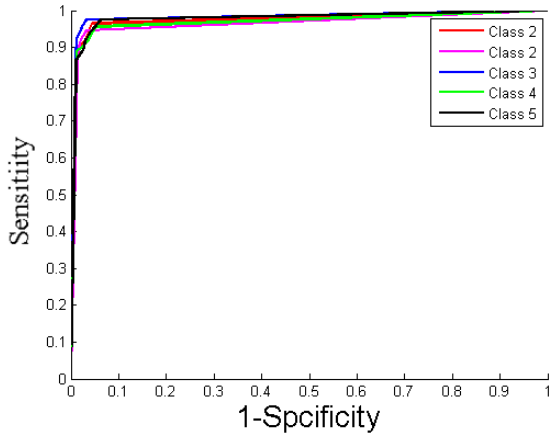

Figure 4: ROC curve for brain tumour classification.

The measures of Accuracy, F1-score, and Cohen-Kappa score are 96%, 0.94, and 0.35.

CONCLUSIONS

The datasets are collected from various hospitals in West Bengal. The results obtained by the proposed approach indicate that there is a variations of sign of abnormalities before and after COVID-19. It also correctly detected the abnormalities, if present. The performance measures such as Accuracy, F1-score and Cohen-Kappa score are calculated for five months and graphically presented in the result section.

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